

SERID NO:31

1127	1127 VVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFG 1176
111	QPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFK:
1227	LLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQS: A3G52 A3G54 A3G52 A3G54 A3G52 A3G54 A3G52 A3G54
1277	SNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLNKPI
1327	VINOLLODTPVASPRSVKVWODACSPLPKTO
1377	POELLKPRSOFAVDMOTTSSRGLVFHTGTKNSFMALYLSKG
1427	OGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRARE
1477	APVYLGSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPS
1527	1527 VSSCLGGPLEKGIYFS 1542 A3G85 A3G88 A3G88

Figure 5

Replace ment sheet

SERID NO: 32

TSISLYMKPPPKPOTTGAWVADOPVLYLGSKNAKKEYHGLAIKNDNLVYVYNLGHKDVEILLDSKPVSSWPAYFSIV A4G-1 A4G-2 A4G-3 A4G-4 A4G-5 A4G-6 A4G-7 A4G-8 A4G-9 A4G-10 P29
KIERVGKHGKVFLTVPSSSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL

A4G-11 A4G-12 A4G-13 A4G-14 A4G-15 A4G-16 A4G-17 A4G-18 A4G-19 1006 NNDVISLYNFKHIYNMDPSKSYPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQVTRFDIEIRTPADNGLV A4G-22 A4G-23 A4G-24 A4G-25 A4G-26 A4G-27 A4G-28 1159 LLHVNGSHFFSLEHRNGYLHVFYDFGFSNGPVHLEDTLKKAQINDAKYREISIIYENDKKHILVVDRRHVKSTDNEK A4G-29 A4G-30 A4G-31 A4G-32 A4G-33 A4G-34 A4G-35 A4G-36 A4G-37 1146 KKIPFTDIYIGGAPQEVLQSRTLRAHLPLDINFRGCMKGIQFQKKDFNLLEQTETLGVGYGCPEDSLISRRAYFNGQ A4G-38 A4G-39 A4G-40 A4G-41 A4G-42 A4G-43 A4G-44 A4G-45 A4G-46 A4G-47 121) SPIASIQKISPFDGPEGGFNFRTLQPNGLLFYYTSGSDVFSISLDNGTVVNDVKGIKVHSTDKQYHDGLPHPVVTSI A4G-48 A4G-49 A4G-50 A4G-51 A4G-52 A4G-53 A4G-54 A4G-55 A4G-56 1336 SDTRYELVVDKSRLRGKNPTKGKAEQTOTTEKKPYFGGSPISPQYANFTGCISNAYFTRLDRDVEVEAFQRYSEKVH A4G-57 A4G-58 A4G-59 A4G-60 A4G-61 A4G-62 A4G-63 A4G-64 A4G-65 A4G-66 TSLYECPIESSPLFLLHXXGKNSSKPKTNKQGEKSKDAPSWDPIGLKFLEQKAPRDSHCHLFSSPRAIEHAYQYGGT

A4G-67 A4G-68 A4G-69 A4G-70 A4G-71 A4G-72 A4G-73 A4G-74 A4G-75 ansrqepeheqgopgeksqpsirlktrsshgmifyvsdqeendfhtlplahgrlvphphvghkklkirsqekyndgl A4G-76 A4G-77 A4G-78 A4G-79 A4G-80 A4G-81 A4G-82 A4G-83 A4G-84 A4G-85 1621 WHDVIFIREKSSGRLVIDGLRVLEERLPPSGAAWKIKGPIYLGGVAPGRAVKNVQITSVYSFSGCLGNLQLNGASIT A4G-86 A4G-87 A4G-88 A4G-89 A4G-90 A4G-91 A4G-92 A4G-93 1622 SASQTPSVTPCFEGPMETGTYFSTEGGYVVLDESFNIGLKPEIAFEVRPRSSSGTLVEGHSVNGEYLNVEHRNGQVI A4G-95 A4G-96 A4G-97 A4G-98 A4G-99 A4G-100 A4G-101 A4G-102 A4G-103 1699 VKVNNGVRDFSTSVTPKQNLCDGRWHRITVIRDSNVVQLDVDSEVNHVVGPLNPKPVDHREPVFVGGVPESLLTPRL A4G-104 A4G-105 A4G-106 A4G-107 A4G-108 A4G-109 A4G-110 A4G-111 A4G-112 1776 APSKPFTGCIRHFVIDSRPVSFSKAALVSGAVSINSCPTA A4G-113 A4G-114 A4G-115 A4G-116

Figure 6

SEQID NO: 33

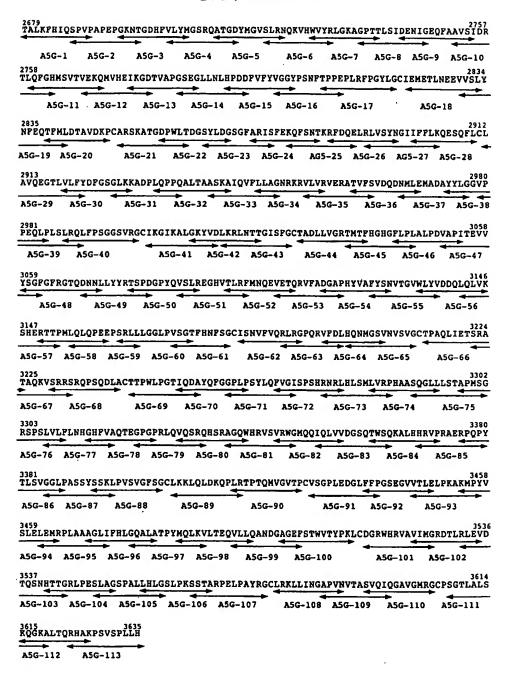


Figure 7

÷	PEPTIDES	Laminin Chain and Amino Acid Sequence Number	Amino Acid Sequence	% Disruption/ Disassembly of Fibrilla AB (AB: Peptide Mola Ratio of 1:6)	
	AG73	Alpha-1 chain; residues 2719-2730	RKRLQVQLSIRT	46 % (S; p < 0.01)***	No: 1
	A3	Alpha-3 chain; residues 2243-2254	KPRLQFSLDIQT	23 % (S; p < 0.01)	NO:20
	A5	Alpha-5 chain; residues 3275-3286	RNRLHLSMLVRP	22 % (S; p<0.01)	NO:21
	C-16	Gamma-1 chain; residues 139-150	KAFDITYVRLKF	28 % (S; p<0.01)***	NO:Z
	LAM-L	Alpha-1 chain; residues 2097-2108	AASIKVAVSADR	24 % (S; p<0.01)	No:ZZ
	A-13	Alpha-1 chain; residues 97-109	RQVFQVAYIIIKA	30 % (S; p<0.01)***	NO: 3
	HA3G45	Alpha-3 chain; residues 1173-1184	ASFGFQTFQPSG	21 % (S; p<0.05)	NO:23
	HA3G47	Alpha-3 chain; residues 1189-2000	HQTWTRNLQVTL	28 % (S; p<0.01)***	No: 4
	HA3G58	Alpha-3 chain; residues 1276-1287	ISNVFVQRLSLS	32 % (S; p<0.01)***	NO. S
	HA3G67	Alpha-3 chain; residues 1342-1353	ASPPSVKVWQDA	25 % (S; p<0.01)***	NO: 6
	HA3G71	Alpha-3 chain; residues 1379-1390	FKLPQELLKPRS	23 % (S; p<0.05)	NO:ZY
	HA3G74	Alpha-3 chain; residues 1402-1414	RGLVFHTGTKNSF	32 % (S; p<0.01)***	NO: 7
	HA3G75	Alpha-3 chain; residues 1411-1422	KNSFMALYLSKG	24 % (S; p<0.01)	No:25
	HA3G76	Alpha-3 chain; residues 1418-1429	YLSKGRLVFALG	26 % (S; p<0.01)***	16:8
•	HA3G79	Alpha-3 chain; residues 1444-1455	NDGKWHTVVFGH	27 % (S; p<0.01)***	NO: 9
	HA3G83	Alpha-3 chain; residues 1477-1487	GNSTISIRAPVY	33 % (S; p<0.01)***	NO:10
	A4G31	Alpha-4 chain; residues 1101-1112	LHVFYDFGFSNG	23 % (S; p<0.01)	No:26
	A4G82	Alpha-4 chain; residues 1513-1524	TLFLAHGRLVFM	30 % (S; p<0.01)***	NO:11
	A5G15	Alpha-5 chain; residues 2792-2803	HPDDFVFYVGGY	30 % (S; p<0.01)***	NO:12
	A5G35	Alpha-5 chain; residues 2950-2961	VLVRVERATVFS	20 % (S; p<0.05)	10:27
	A5G46	Alpha-5 chain; residues 3043-3054	FLPLALPDVAPI	21 % (S; p<0.05)	W: 28
	A5G56	Alpha-5 chain; residues 3135-3146	WLYVDDQLQLVK	27 % (S; p<0.01)***	16:13
	A5G71	Alpha-5 chain; residues 3259-3270	GPLPSYLQFVGI	22 % (S; p<0.05)	ND: 29
	A5G80	Alpha-5 chain; residues 3329-3340	VQSRQHSRAGQW	25 % (S; p<0.01)***	NO: 14
	A5G81	Alpha-5 chain; residues 3337-3348	AGQWHRVSVRWG	41 % (S; p<0.01)***	10:15
	A5G82	Alpha-5 chain; residues 3345-3356	VRWGMQQIQLVV	29 % (S; p<0.01)***	10:16
	A5G84	Alpha-5 chain; residues 3361-3372	TWSQKALHHRVP	27 % (S; p<0.01)***	20:17
	A5G101	Alpha-5 chain; residues 3516-3527	DGRWHRVAVIMG	39 % (S; p<0.01)***	NO:18
	A5G109	Alpha-5 chain; residues 3587-3598	APVNVTASVQIQ	32 % (S; p<0.01)***	NO: 19
	A5G110	Alpha-5 chain; residues 3594-3605	SVQIQGAVGMRG	23 % (S; p<0.05)	NO:30

*** Selected for Further Testing

Figure 8

	SERIDNO	Structure	Formula	MW
DP-001 D-AG73 or D-A1 A1-chain 2719-2730	No:1	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr	C ₆₄ H ₁₂₀ N ₂₄ O ₁₇	1497.82
DP-002 D-A13 A1-chain 97-109	N0:3	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala	C74H121N19O17	1548.90
DP-003 D-HA3G76 A3-chain 1418-1429	No:8	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly	C ₆₃ H ₁₀₂ N ₁₆ O ₁₅	1323.61
DP-004		Thr-Leu-Phe-Leu-Ala-His-Gly-Arg-Leu-Val-Phe-Met		
D-A4G82 A4-chain 1513-1524	No: _I I	MAN AND AND AND AND AND AND AND AND AND A	C ₆₇ H ₁₀₅ N ₁₇ O ₁₄ S	1404.75
DP-005 D-A5G81 A5-chain 3337-3348	No:15	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly	C ₆₅ H ₉₅ N ₂₃ O ₁₅	1438.62
DP-006 D-A5G101 A5-chain . 3516-3527	No: 18	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly	C ₆₁ H ₉₇ N ₂₁ O ₁₅ S	1396.65
DP-007 D-HA3G47 A3-chain 1189-2000	No. 4	His-Gln-Thr-Trp-Thr-Arg-Asn-Leu-Gln-Val-Thr-Leu	C ₆₆ H ₁₀₅ N ₂₁ O ₁₉	1496.70
DP-008 P-HA3G58 A3-chain 1276-1287	NO:5	Ile-Ser-Asn-Val-Phe-Val-Gln-Arg-Leu-Ser	C ₆₁ H ₁₀₃ N ₁₇ O ₁₈	1362.60

Fig. 12a

PTI-	SECIDNO	Structure	Formula	MW
DP-009 D-HA3G74 A3-chain 1402-1414	No: 7	Arg-Gly-Leu-Val-Phe-His-Thr-Gly-Thr-Lys-Asn-Ser-Phe	C ₆₆ H ₁₀₂ N ₂₀ O ₁₈	1463.67
DP-010 D-HA3G83 A3-chain 1477-1487	No: 10	Gly-Asn-Ser-Thr-Ile-Ser-Ile-Arg-Ala-Pro-Val-Tyr	C ₅₆ H ₉₂ N ₁₆ O ₁₈	1277.45
DP-011 D-A5G82 A5-chain 3345-3356	No:16	Val-Arg-Trp-Gly-Met-Gln-Gln-Ile-Gln-Leu-Val-Val	: C ₆₆ H ₁₀₉ N ₁₉ O ₁₆ S	1456.78
DP-012 D-A5G109 A3-chain 1444-1455	No: 19	Ala-Pro-Val-Asn-Val-Thr-Ala-Ser-Val-Gln-Ile-Gln	C53H91N15O18	1226.40
DP-013 D-rAG73 or D-rA1 A1-chain r2719-2730 or	NO:34	Thr-Arg-Ile-Ser-Leu-Gln-Val-Gln-Leu-Arg-Lys-Arg	C ₆₄ H ₁₂₀ N ₂₄ O ₁₇	1497.82
2730-2719 DP-014 D-rA13 A1-chain r92-109 or 109-92	No:35	Ala-Lys-Ile-Ile-Ile-Tyr-Ala-Val-Gln-Phe-Val-Gln-Arg	C74H121N19O17	1547.92
DP-015 D-rHA3G76 A3-chain r1418-1429 or 1429-1418		Gly-Leu-Ala-Phe-Val-Leu-Arg-Gly-Lys-Ser-Leu-Tyr	C ₆₃ H ₁₀₂ N ₁₆ O ₁₅	1323.61
DP-016 D-rA4G82 A4-chain r1513-1524 or 1524-1513	No.36 No:37	Met-Phe-Val-Leu-Arg-Gly-His-Ala-Leu-Phe-Leu-Thr	C ₆₇ H ₁₀₅ N ₁₇ O ₁₄ S	1404.75

Fig. 126

DYPY	Cc0.70 .10			
PTI- DP-017	SEQIO NO	Structure Structure	Formula	MW
DP-017 D-rA5G81 A5-chain r3337-3348 or 3348-3337		Gly-Trp-Arg-Val-Ser-Val-Arg-His-Trp-Gln-Gly-Ala	C ₆₅ H ₉₅ N ₂₃ O ₁₅	1438.62
DP-018 D-rA5G101 A5-chain r3516-3527 or 3527-3516		Gly-Met-Ile-Val-Ala-Val-Arg-His-Trp-Arg-Gly-Asp	C ₆₁ H ₉₇ N ₂₁ O ₁₅ S	1396.65
LP-019 AG73 or AI AI-chain 2719-2730	NO: 1	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr	C ₆₄ H ₁₂₀ N ₂₄ O ₁₇	1497.82
LP-020 A13 A1-chain 92-109	No:3	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala	C74H121N19O17	1548.90
LP-021 HA3G76 A3-chain 1418-1429	No: 8	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly	C ₆₃ H ₁₀₂ N ₁₆ O ₁₅	1323.61
	No:40	HOW TON	C ₆₇ H ₁₀₅ N ₁₇ O ₁₄ S	1404.75
LP-023 A5G81 A5-chain 3337-3348	No! 15	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly	C ₆₅ H ₉₅ N ₂₃ O ₁₅	1438.62
LP-024 A5G101 A5-chain 3516-3527	NO:18	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly	C ₆₁ H ₉₇ N ₂₁ O ₁₅ S	1396.65

Fig. 12c

PTI-	SERIO NO	Structure	Formula	MW
LP-025		Leu-Pro-Phe-Phe-Asp		
β-sheet breaker	<u> </u>			(0
or		HOW YOU WAY YOU CAN	C ₃₃ H ₄₃ N ₅ O ₈	637.74
іАβ5				
	NO:41		·	,
DP-026		Ala-Gly-Gln-Trp-His-Arg-Val	. '	
Trc'n		wid is said		
5;1-7			C ₃₈ H ₅₆ N ₁₄ O ₉	852.95
	No:42			
DP-027	100:70	Gly-Gln-Trp-His-Arg-Val-Ser		
Trc'n		Siy-Oii-Tip-Tiis-Aig-Vai-Sei		
5;2-8			C38H56N14O10	868.95
,				
	No:43		•	
DP-028		Gln-Trp-His-Arg-Val-Ser-Val		
Trc'n			,	, and the second
5;3-9		701 701 COI	C ₄₁ H ₆₂ N ₁₄ O ₁₀	911.04
	475			
	No:44	IN Ant		
DP-029		Trp-His-Arg-Val-Ser-Val-Arg		
Trc'n 5;4-10		and the state of t	C ₄₂ H ₆₆ N ₁₆ O ₉	939.09
3,4-10			C42116611[6C9	
	NO:45			
DP-030		His-Arg-Val-Ser-Val-Arg-Trp		
Trc'n	·			939.09
5;5-11			C ₄₂ H ₆₆ N ₁₆ O ₉	939.09
:	12.11			
	No:41	100		
DP-031	.]	Arg-Val-Ser-Val-Arg-Trp-Gly		•
Trc'n 5;6-12		and the fact of the same of th	C ₃₈ H ₆₂ N ₁₄ O ₉	859.00
J,U-12			3002-14-9	
	No: 47		[·	
DP-032		Asp-Gly-Arg-Trp-His-Arg-Val	 	
Trc'n				
6;1-7		HAN JOHN JOHN JOHN JOHN JOHN JOHN JOHN JOH	C ₄₀ H ₆₀ N ₁₆ O ₁₀	925.02
				•
Ì	No: 48	ON NOT THE REP.		
•	•	Ma and A ma	•	

Fig. 12d

PTI-	SERTO NO	Structure	Formula	MW
DP-033	LCMTA WO	Gly-Arg-Trp-His-Arg-Val-Ala		
Trc'n	·			004.04
6;2-8		Ho Marian	$C_{39}H_{60}N_{16}O_8$	881.01
			į	
T C C C C C C C C C C C C C C C C C C C	NO:49	NO NOT NOT NOT NOT NOT NOT NOT NOT NOT N		
DP-034		Arg-Trp-His-Arg-Val-Ala-Val		
Trc'n		i l had i s		000.00
6;3-9		AND THE COM	C ₄₂ H ₆₆ N ₁₆ O ₈	923.09
	No:50	the way the	·	
DP-035		Trp-His-Arg-Val-Ala-Val-Ile	*	
Trc'n			C ₄₂ H ₆₅ N ₁₃ O ₈	880.07
6;4-10	,		0421263111308	
	NO:51			
DP-036	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	His-Arg-Val-Ala-Val-Ile-Met		
Trc'n				
6;5-11		B. W. 1984 1984 1984	C ₃₆ H ₆₄ N ₁₂ O ₈ S	825.05
				•
	NO:52	Bry Nite		
DP-037		Arg-Val-Ala-Val-Ile-Met-Gly		
Trc'n		and the state of t	C ₃₂ H ₆₀ N ₁₀ O ₈ S	744.96
6;6-12		1 / / / / / /	C3211601110080	
	10:53	3—		*
DP-038		Thr-Leu-Phe-Leu-Ala-His-Gly	·	
Trc'n		and I had I go		757.00
4;1-7	٠.	And the second of the second o	C ₃₆ H ₅₅ N ₉ O ₉	757.89
	No: 54			
DP-039	, , ,	Leu-Phe-Leu-Ala-His-Gly-Arg		
Trc'n		1 Indian indian		010.07
4;2-8		604 2017 I July 101 201	$C_{38}H_{60}N_{12}O_8$	812.97
		70 0		
	No:55	in the state		
DP-040		Phe-Leu-Ala-His-Gly-Arg-Leu		
Trc'n		I have been a little and little a		812.98
4;3-9	·	HON'S TON	$C_{38}H_{60}N_{12}O_{8}$	012.70
	Nb: 56	100 Sto		9
•	1	Fig. 12e	1	

PTI-	SERID NO	Structure	Formula	MW
DP-041		Leu-Ala-His-Gly-Arg-Leu-Val		
Trc'n		LIMI		
4;4-10		Way which you have the total	C ₃₄ H ₆₀ N ₁₂ O ₈	764.93
	No:57	acra nac		
DP-042	100:31	Ala-His-Gly-Arg-Leu-Val-Phe		
Trc'n	·	Ala-Mis-Gly-Alg-Lea-Vall-Inc		
4;5-11			C ₃₇ H ₅₈ N ₁₂ O ₈	798.95
.,	NO:58	4 1 4 . 0		
DD 040		TV: Clu Are Lee Vol Dhe Met		
DP-043		His-Gly-Arg-Leu-Val-Phe-Met		
Trc'n 4;6-12			C ₃₉ H ₆₂ N ₁₂ O ₈ S	859.07
4,0-12		4 3 7 ~ 70 ~		
	NO:59			
DP-044		Gly-Leu-Ala-Phe-Val-Leu-Arg		
Trc'n			C ₃₇ H ₆₂ N ₁₀ O ₈	774.97
15;1-7		m \ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	C3711621110O8	
8	NO:60			
DP-045		Leu-Ala-Phe-Val-Leu-Arg-Gly		
Trc'n				55. 05.
15;2-8	·		$C_{37}H_{62}N_{10}O_8$	774.97
0.15	NO:61	10		
DP-046	(Ala-Phe-Val-Leu-Arg-Gly-Lys		
Trc'n 15;3-9			C ₃₇ H ₆₃ N ₁₁ O ₈	789.98
13,3-3		$\langle \langle \cdot \rangle \rangle$	03/110311108	
	20.15	` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` ` `		
DP-047	NO:62	Phe-Val-Leu-Arg-Gly-Lys-Ser		
Trc'n		File-Val-Led-Aig-Oiy-Lys-oci		
15;4-10		RAN TORK TORK TORK	C ₃₇ H ₆₃ N ₁₁ O ₉	805.98
20,120			•	
	NO:63	te hou	. 1	
DP-048		Val-Leu-Arg-Gly-Lys-Ser-Leu		
Trc'n		" A R " A R		. •
15;5-11		MILL MILL MILL MILL MILL MILL MILL MILL	C ₃₄ H ₆₅ N ₁₁ O ₉	771.96
,		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	3,,	
	10.64	, in		-
	NO:64	MH2 MH2		
DP-049	Ī	Leu-Arg-Gly-Lys-Ser-Leu-Tyr		
Trc'n		Lles a Lla		026.03
15;6-2		HEN YOU YOU NOW YOU NOW	$C_{38}H_{65}N_{11}O_{10}$	836.01
	Ì	7 3 3 4 7 0		
	No:65	Mary State State		
	<u> </u>	Eig 13f	<u> </u>	

Fig. 12f